

Score: 43.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 5.93%
DB: 6
Matches: 43
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-735-098-2 (1-725) x BD074758 (1-2262)

QY 171 ArgLeuGIYTYrApGIYpHeValTYTYrSerGIYGLuArProSerGIInSerLeuPro 150
DB 526 CGCTTACGTATGACGGCTTTGTATATTATTCGGGAAAGCTCTTCCCATCTTACCG 585
QY 191 SerAlaGIYThrAlaGIYTYrSerGIYAsnTYrGlnTYrMetThrAlaAlaYsArgHis 210
DB 586 AGTGGCGGAAACGGTGAATTCCTGTACTGCAATATATGACCAATGCCAAACGTCAT 645
QY 211 ArgAlaGIY 213
DB 646 CGAGCAGGT 654

RESULT 22
AF072890 2519 bp DNA linear BCT 22-JAN-1999

LOCUS AF072890 Neisseria gonorrhoeae lactoferrin binding protein B precursor
DEFINITION (lbpB) gene, complete cds.
ACCESSION AF072890
VERSION AF072890.1 GI:4106392
KEYWORDS
SOURCE Neisseria gonorrhoeae
ORGANISM Neisseria gonorrhoeae
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.

REFERENCE 1 Bivas, G.D., Anderson, J.E., Eben, C.J., Cornelissen, C.N. and Sparling, P.F.
AUTHORS Identification and functional characterization of the Neisseria
gonorrhoeae lbpB gene product
JOURNAL Infect. Immun. 67 (1), 455-459 (1999)
MEDLINE 99081783
PUBMED 9864256
2 (bases 1 to 2519)
REFERENCE Bivas, G.D., Anderson, J.E., Cornelissen, C.N. and Sparling, P.F.
AUTHORS Direct Submission
TITLE Submitted (18-JUN-1998) Medicine/ID, Univ. of N. Carolina, 521
JOURNAL Burnett Womack/CB 7030, Chapel Hill, N.C. 27599, USA
FEATURES
source 1..2519
/organism="Neisseria gonorrhoeae"
/mol_type="genomic DNA"
/strain="FA19"
/db_xref="taxon:485"
terminator 184..209
/note="putative"
gene 276..2496
/gene="lbpB"
276..293
/gene="lbpB"
/note="putative"
protein_bind 301..304
/bound_molecule="FUR"
310..2496
/gene="lbpB"
310..2496
/gene="lbpB"
/note="lbpB"
/codon_start=1
/transl_table=1
/product="lactoferrin binding protein B precursor"
/protein_id="AA08809.1"
/db_xref="GI:4106393"
/translation="MRKLVYGIALLPLMLASCGNFGVQPEVSTPTAYPVTPKSKD
VPTSPPAEVEVETTPVPRPAVGAAMRLRNTAFPHREDGTAIPDSKQAEKLSFKG
DVLPGSKGNKLOOLKEIKHSDSDVEIRSEKENVKGYEVPDAGVYTRNKDEI
EONGGKRFTHRFYDGFVYISGRPSGLSAQTVKFGMWQYMTDAKRHTGAAVA

RBS
CDS

FEATURES
source 1..2519
/organism="Neisseria gonorrhoeae"
/mol_type="genomic DNA"
/strain="FA19"
/specific_host="Homo sapiens"

142

ORIGIN

Alignment Scores:
Pred. No.: 9/226-35
Score: 41.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 5.66%
DB: 1
Length: 2519
Matches: 41
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-735-098-2 (1-725) x AF072890 (1-2519)

QY 101 GluGIYAspValLeuPheLeuTYrGIYSerLYSGIYAsnLYLeuGlnLeuLYsSer 120
DB 610 GAAGGTGAGTTCCTCTTTTATACCGTTCAGAAAGAAATTAACCTTCACACTTAAAC 669
QY 121 GluLeuHsLYrAspAspSerAspValGluLeuTYrSerGIYLYSGIYAsnLYsLYs 140
DB 670 GAAATTCATTAACGTAATTCGATGTAGAAATTAGACGTCGAAAGGAAATTAATAA 729
QY 141 TYr 141
DB 730 TAT 732

RESULT 23
NGU16260 3300 bp DNA linear BCT 27-FEB-1996
LOCUS NGU16260
DEFINITION Neisseria gonorrhoeae lactoferrin receptor precursor (lbpA) gene,
complete cds.
ACCESSION U16260
VERSION U16260.1 GI:915277
KEYWORDS
SOURCE Neisseria gonorrhoeae
ORGANISM Neisseria gonorrhoeae
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.

REFERENCE 1 Bivas, G.D. and Sparling, P.F.
AUTHORS Characterization of lbpA, the structural gene for a lactoferrin
TITLE receptor in Neisseria gonorrhoeae
JOURNAL Infect. Immun. 63 (8), 2958-2967 (1995)
MEDLINE 95347808
PUBMED 7622218
2 (bases 1 to 3300)
REFERENCE Bivas, G.D.
AUTHORS Direct Submission
TITLE Submitted (24-OCT-1994) Gour D. Bivas, Dept. of Medicine/Div. of
JOURNAL Intec. Dis., University of North Carolina, 521 Burnett-Womack
CB#7030, Chapel Hill, NC 27599-7030, USA
FEATURES
source 1..3300
/organism="Neisseria gonorrhoeae"
/mol_type="genomic DNA"
/strain="FA19"
/specific_host="Homo sapiens"

B15wv5p9.1

[illegible]

AUTHORS	Berthel, F.X., Lobet, Y., Poolman, J. and Verlant, V.				
TITLE	Chlamydia vaccine composition				
JOURNAL	Patent: WO 02062380-A 80 15-AUG-2002; Glaxosmithkline Biologicals (BE)				
FEATURES	Location/Qualifiers				
source	1. .3300 /organism="Neisseria gonorrhoeae" /mol_type="unassigned DNA" /db_xref="taxon:485"				
ORIGIN					
Alignment Scores:					
Pred. No.:	2.3e-13	Length:	3300		
Score:	22.00	Matches:	22		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	3.03%	Indels:	0		
DB:	6	Gaps:	0		
US-10-735-098-2 (1-725) x AX685922 (1-3300)					
QY	704	PROGLUVALYSPROGINPHGILVALALPHGILVALALYSASPANLYSGILVAL	723		
Db	213	CGGAAGTTAAACCCCAATTCGGCGTGTATTCGGTCCGAAGAAAGATATTAAGAGGTG	272		
QY	724	GLULYS	725		
Db	273	GAATAA	278		
RESULT 25					
AX081510	AX081510	1000 bp	DNA	linear	PAT 27-FEB-2001
LOCUS	Sequence 15 from Patent WO0109350.				
DEFINITION	AX081510				
ACCESSION	AX081510				
VERSION	AX081510.1	GI:13170329			
KEYWORDS					
SOURCE	Neisseria meningitidis				
ORGANISM	Neisseria meningitidis				
	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;				
	Neisseriaceae; Neisseria.				
REFERENCE	1				
AUTHORS	Berthel, F.X., Dalemans, W.L., Denoel, P., Deguesne, G.S., Feron, C.S.,				
	Lobet, Y.S., Poolman, J.S., Thiry, G.S., Lhonnard, J.S. and Voet, P.S.				
TITLE	Genetically engineered bled vaccine				
JOURNAL	Patent: WO 0109350-A 15 08-FEB-2001,				
	SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)				
FEATURES	Location/Qualifiers				
source	1. .1000 /organism="Neisseria meningitidis" /mol_type="unassigned DNA" /db_xref="taxon:487"				
ORIGIN					
Alignment Scores:					
Pred. No.:	1.26e-11	Length:	1000		
Score:	20.00	Matches:	20		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	2.76%	Indels:	0		
DB:	6	Gaps:	0		
US-10-735-098-2 (1-725) x AX081510 (1-1000)					
QY	427	ALACYSASAPHELEUTHRYVALYSLHUGLYARGILEYRTHGLUARGFROALA	446		
Db	106	GCTGTGTCGACCTTTTGACCTAAGTGAACCTCGGACGATMAAAACCGAAGCGCCGCA	165		
RESULT 26					
AX374691	AX374691	1000 bp	DNA	linear	PAT 01-MAR-2002
LOCUS	Sequence 15 from Patent WO0209746.				
DEFINITION	AX374691				
ACCESSION	AX374691				
VERSION	AX374691.1	GI:19169587			

ment Scores:

No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
0.0171	2040	13	0	0	0	0
13.00						
100.00%						
100.00%						
1.79%						

0-735-098-2 (1-725) x AAX26576 (1-2040)

649 GYGLYPhETyRGlyProLYsAlaGluGluLeuGlyGly 661
 1882 GCGCGTTTACGGGCGCTAAAGCCGAAGATTGGCGCGG 1920

14-JUN-1999 (first entry)
 AAX26577 standard; DNA; 2058 BP.

14-JUN-1999 (first entry)

TdpB coding sequence from Neisseria meningitidis strain 8680.

Low molecular weight subunit; TdpB; human transferrin receptor; hTR; Neisseria meningitidis; vaccine; meningococcal infection; meningitis; ss.

Neisseria meningitidis.

Key	Location/Qualifiers
CDS	1..2058
sig_peptide	/*tag= a
mat_peptide	1..48
	/*tag= b
	49..2058
	/*tag= c

MO9907741-A1.

18-FEB-1999.

03-AUG-1998; 98MO-FR001730.

07-AUG-1997; 97FR-00010301.

(INNER) PASTEUR MERIEUX SERUMS & VACCINS SA.

Quentin-Millet M, Rokbi B;

WPI; 1999-190036/16.

P-PSDB; AAY01525.

Vaccine containing small subunit of human transferrin receptor from Neisseria meningitidis - for treatment and prevention of meningitis.

Disclosure; Page 40-43; 73pp; French.
 The present sequence encodes the low molecular weight subunit (TdpB) of the human transferrin receptor (hTR) from a specific strain of Neisseria meningitidis that contains TdpB-encoding DNA. Compositions containing TdpB are used as vaccines for treatment or prevention of meningococcal infections, particularly meningitis

Sequence 2058 BP; 621 A; 477 C; 551 G; 409 T; 0 U; 0 Other;

Alignment Scores:

Seq. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
0.0172	2058	13	0	0	0	0
13.00						
100.00%						
100.00%						
1.79%						

US-10-735-098-2 (1-725) x AAX26577 (1-2058)

QY 649 GYGLYPhETyRGlyProLYsAlaGluGluLeuGlyGly 661
 DB 1900 GCGCGTTTACGGGCGCTAAAGCCGAAGATTGGCGCGG 1938

RESULT 20
 AAT11243
 ID AAT11243 standard; DNA; 2070 BP.

AC AAT11243;

DT 16-OCT-2003 (revised)

DT 02-SEP-1996 (first entry)

DE Neisseria meningitidis strain B283 transferrin receptor Tdp2 gene.

XX Transferrin receptor; Tdp2 subunit; deletion mutant; vaccine;

XX Passive immunisation; immunotherapy; IM2169; IM2394; ss.

OS Neisseria meningitidis; (strain B283).

Key	Location/Qualifiers
CDS	1..2070
sig_peptide	/*tag= a
mat_peptide	1..60
	/*tag= b
	61..2067
	/*tag= c

MO9531040-A2.

07-DEC-1995.

30-MAY-1995; 95MO-FR000701.

31-MAY-1994; 94FR-00006594.

(INNER) PASTEUR MERIEUX SERUMS & VACCINS.

(TRGE) TRANSGENE SA.

Millet MBU, Lissolo L, Mazarin V, Legrain M, Jacobs E;

WPI; 1996-030562/03.

P-PSDB; AAR8648.

Polypeptide(s) for vaccination against Neisseria meningitidis group B - comprising deletion mutants of transferrin receptor Tdp2 subunit.

Disclosure; Page 76-81; 114pp; French.

The present sequence is that of the N.meningitidis strain B283 transferrin Tdp2 subunit gene. The Tdp2 polypeptide has three domains: an N-terminal domain, a hinge domain and a C-terminal domain; deletion mutants in which at least one of the domains is partially or totally deleted are claimed, provided that the first and second domains are not simultaneously partially or totally deleted. The positions of the 3 CC domains in B283 are defined by alignment with the IM2169 sequence. The deletion mutant polypeptides of the invention can generate an immune response against N.meningitidis. (Updated on 16-OCT-2003 to standardise CC OS field)

Sequence 2070 BP; 617 A; 472 C; 560 G; 421 T; 0 U; 0 Other;

Alignment Scores:

Seq. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
0.0173	2070	13	0	0	0	0
13.00						
100.00%						
100.00%						
1.79%						

Millet MBU

US-10-735-098-2 (1-725) x AAT11243 (1-2070)
 QY 649 G1yG1yPheTyG1yProTySaLaG1uG1uLeuG1yG1y 661
 DB 1912 GCGGGTTTACGGCCCTTAAGCCGAAGAGTTGGCGGA 1950

RESULT 21

AAT11241 standard; DNA; 2114 BP.

AAT11241;

16-OCT-2003 (revised)

02-SEP-1996 (first entry)

Neisseria meningitidis strain 6940 transferrin receptor Tbp2 gene:

Transferrin receptor; Tbp2 subunit; deletion mutant; vaccine;
 passive immunisation; immunotherapy; IM2169; ss.

Neisseria meningitidis; (strain 6940).

Key Location/Qualifiers

CDS 1..2082

FT 1..2079

mat_peptide 1..2079

/*tag= b

W09533049-A2.

07-DEC-1995.

30-MAY-1995; 95MO-FR000701.

31-MAY-1994; 94FR-00006594.

(INNER) PASTEUR MERIEUX SERUMS & VACCINS.

(TRGE) TRANSGENE SA.

Milliet MBJ, Lisolo L, Mazarin V, Legrain M, Jacobs E;

WPI; 1996-030562/03.

P-PSDB; AAR88646.

Polypeptide(s) for vaccination against Neisseria meningitidis group B -

comprising deletion mutants of transferrin receptor Tbp2 subunit.

Disclosure; Page 53-56; 114pp; French.

The present sequence is that of the N.meningitidis strain 6940

transferrin Tbp2 subunit gene. The Tbp2 polypeptide has three domains: an

N-terminal domain, a hinge domain and a C-terminal domain; deletion

mutants in which at least one of the domains is partially or totally

deleted are claimed, provided that the first and second domains are not

simultaneously partially or totally deleted. Strain 6940 is an IM2169-

related N.meningitidis strain and the positions of the 3 domains are

defined by alignment with the IM2169 sequence. The deletion mutant

polypeptides of the invention can generate an immune response against

N.meningitidis. (Updated on 16-OCT-2003 to standardise OS field)

Sequence 2114 BP; 695 A; 478 C; 511 G; 430 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.0177 Length: 2114

Score: 13.00 Matches: 13

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.79% Indels: 0

DB: 2 Gaps: 0

US-10-735-098-2 (1-725) x AAT11241 (1-2114)

QY 649 G1yG1yPheTyG1yProTySaLaG1uG1uLeuG1yG1y 661

DB 1942 GCGGGTTTACGGCCCTTAAGCCGAAGAGTTGGCGGA 1950

DB 1936 GCGGGTTTACGGCCCTTAAGCCGAAGAGTTGGCGGA 1974

RESULT 22

AAT11242 standard; DNA; 2114 BP.

AAT11242;

16-OCT-2003 (revised)

02-SEP-1996 (first entry)

Neisseria meningitidis strain S3032 transferrin receptor Tbp2 gene:

Transferrin receptor; Tbp2 subunit; deletion mutant; vaccine;
 passive immunisation; immunotherapy; IM2169; ss.

Neisseria meningitidis; (strain S3032).

Key Location/Qualifiers

CDS 1..2100

FT 1..2097

mat_peptide 1..2097

/*tag= b

W09533049-A2.

07-DEC-1995.

30-MAY-1995; 95MO-FR000701.

31-MAY-1994; 94FR-00006594.

(INNER) PASTEUR MERIEUX SERUMS & VACCINS.

(TRGE) TRANSGENE SA.

Milliet MBJ, Lisolo L, Mazarin V, Legrain M, Jacobs E;

WPI; 1996-030562/03.

P-PSDB; AAR88647.

Polypeptide(s) for vaccination against Neisseria meningitidis group B -

comprising deletion mutants of transferrin receptor Tbp2 subunit.

Disclosure; Page 58-61; 114pp; French.

The present sequence is that of the N.meningitidis strain S3032

transferrin Tbp2 subunit gene. The Tbp2 polypeptide has three domains: an

N-terminal domain, a hinge domain and a C-terminal domain; deletion

mutants in which at least one of the domains is partially or totally

deleted are claimed, provided that the first and second domains are not

simultaneously partially or totally deleted. Strain S3032 is an IM2169-

related N.meningitidis strain and the positions of the 3 domains are

defined by alignment with the IM2169 sequence. The deletion mutant

polypeptides of the invention can generate an immune response against

N.meningitidis. (Updated on 16-OCT-2003 to standardise OS field)

Sequence 2114 BP; 691 A; 493 C; 509 G; 421 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.0177 Length: 2114

Score: 13.00 Matches: 13

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.79% Indels: 0

DB: 2 Gaps: 0

US-10-735-098-2 (1-725) x AAT11242 (1-2114)

QY 649 G1yG1yPheTyG1yProTySaLaG1uG1uLeuG1yG1y 661

DB 1942 GCGGGTTTACGGCCCTTAAGCCGAAGAGTTGGCGGA 1980

Iron uptake protein; transferrin binding protein; TbpA; TbpB; vaccine;
neisserial disease; meningococcal disease; gonococcal disease;
antimicrobial; antibacterial; ds.

Neisseria meningitidis.

Location/Qualifiers
Key 1.2139
/tag= a
/product= "Neisseria meningitidis TbpB protein"

W0200173080-A2.

04-OCT-2001.

27-MAR-2001; 2001WO-GB001348.

27-MAR-2000; 2000GB-00007433.

(MICR-) MICROBIOLOGICAL RES AUTHORITY.

Gorringe AR, Hudson MJ, Matheson MA, Robinson A, West DM,

WPI; 2001-616522/71.

P-PSDB; AAE12019.

Non-neisserial cells useful in manufacturing of vaccines without the loss of antigenicity of the native protein, against meningococcal diseases such as meningitis, express a recombinant neisserial iron uptake protein.

Example 1; Page 19-21; 57pp; English.

The present invention relates to a non-neisserial cell expressing a neisserial iron uptake protein, where neisserial iron uptake proteins including transferrin binding protein (Tbp) A and TbpB can be extracted from the cell under mild conditions and retains substantially the antigenicity of native iron uptake protein. The non-neisserial cell is useful in manufacture of Tbp, and in the manufacture of vaccines for protection against neisserial disease, meningococcal disease and/or gonococcal disease. The affinity matrix is useful for purifying a Tbp, where Tbp containing preparation is eluted through the matrix. The present sequence is a Neisseria meningitidis strain K454 TpbB gene

Sequence 2139 BP; 696 A; 492 C; 519 G; 432 T; 0 U; 0 Other;

Alignment Scores:

Seq. No.:	0.0179	Length:	2139
Percent Similarity:	13.00	Matches:	13
Best Local Similarity:	100.00%	Conservative:	0
Query Match:	100.00%	Mismatches:	0
	1.79%	Indels:	0
	5	Gaps:	0

-10-735-098-2 (1-725) x AAD19530 (1-2139)

649 G|G|G|P|H|E|T|Y|R|G|Y|P|P|O|L|Y|A|L|A|G|I|U|L|E|U|G|Y|G|Y| 661
1993 GCGGTTTTCACGGCCCAAGCCGAAGAGTTGGCGCA 2031

30UT 26

AA055619 standard; DNA; 2230 BP.

AA055619;

16-OCT-2003 (revised)

25-MAR-2003 (revised)

15-JUN-1994 (first entry)

N. meningitidis IM2169 transferrin receptor Tbp2 subunit DNA sequence.

Transferrin receptor; Tbp2 subunit; strain IM2169; meningitis vaccine;

KW Iron transport protein; iron chelator; ss.
XX Neisseria meningitidis; (strain IM2169).
OS

Key Location/Qualifiers

FT CDS 60..2195
FT /tag= a
FT sig_peptide 60..119
FT /tag= b
FT mat_peptide 120..2192
FT /tag= c
FT /product= "Tbp2"

FR2692592-A1.

24-DEC-1993.

19-JUN-1992; 92FR-00007493.

19-JUN-1992; 92FR-00007493.

(INMR) PASTEUR MERIEUX SERUMS & VACCINS.

(TRGE) TRANSENE SA.

Jacobs E, Legrain M, Mazarin V, Bouchon-Theisen B, Shryvers AB;

WPI; 1994-028254/04.

P-PSDB; AAR48222.

DNA coding for neisseria meningitidis proteins - namely transferrin receptor subunits.

Claim 2-7 and 11-12; Page 36-40; 60pp; French.

Sequences coding for the Tbp1 and Tbp2 transferrin receptor subunits were isolated from a Neisseria meningitidis strain IM2169 genomic DNA library (see AA055618 and AA055619, respectively). Cells transformed with the DNA can be used for large scale production of the receptor proteins. (Updated on 25-MAR-2003 to correct PW field.) (Updated on 16-OCT-2003 to standardise OS field)

Sequence 2230 BP; 727 A; 483 C; 547 G; 473 T; 0 U; 0 Other;

Alignment Scores:

Seq. No.:	0.0186	Length:	2230
Score:	13.00	Matches:	13
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.79%	Indels:	0
DB:	2	Gaps:	0

US-10-735-098-2 (1-725) x AA055619 (1-2230)

649 G|G|G|P|H|E|T|Y|R|G|Y|P|P|O|L|Y|A|L|A|G|I|U|L|E|U|G|Y|G|Y| 661
2037 GCGGTTTTCACGGCCCTTAAAGCCGAAGAGTTGGCGCA 2075

RESULT 27

AA011238 standard; DNA; 2230 BP.

AA011238;

16-OCT-2003 (revised)

30-AUG-1996 (first entry)

Neisseria meningitidis strain IM2169 transferrin receptor Tbp2 gene.

Transferrin receptor; Tbp2 subunit; deletion mutant; vaccine;

passive immunisation; immunotherapy; ss.

Neisseria meningitidis; (strain IM2169).

Db	2041	GAAATTGGCGGCTATATTTCCAAAATAATGATGGGAACCTCTTGGTAATACGMAAGATACT	2160
Oy	701	GIUAENGUJALAGIUALAGIUVAIGIUENGLUJALAGIYVALGIYGINLNULYSPRO	720
Db	2101	GAATAATCAAGCTGAGCTGAAGATTCAAATGAACGTGGTGTTGGCGAACATTAACAACCT	2160
Oy	721	GIUALALYSPTSGINPHECGLYVALPHNCGIYALALYSLSYSAAPASLUYGLIUALGIU	740
Db	2161	GAAGCTAATACCCCACAAATTCGGCTGGTATTCGGTCGAAAGAAAGATAAATAAGAAGTGCMA	2220
Oy	741	LYS 741 	
Db	2221	AAT 2223 	

	RESULTS			
	NMLBPAG			
LOCUS	N meningitidis (H44/76)	3398 bp	DNA	linear
DEFINITION	X79838			BCT 06-JUL-1995
ACCESSION	X79838			
VERSION	X79838.1			
KEYWORDS	GI:509053			
SOURCE	lactoferrin binding protein; lbpA gene.			
ORGANISM	Neisseria meningitidis			
	Neisseria meningitidis			
	Neisseria meningitidis			
	Neisseriae; Proteobacteria; Betaproteobacteria; Neisseriales;			
	Neisseriaceae; Neisseria.			
REFERENCE	1			
AUTHORS	*Pettersson A., Klarenbeek V., van Deuren J., Poolman J.T. and Tommassen J.			
TITLE	Molecular characterization of the structural gene for the lactoferrin receptor of the meningococcal strain H44/76			
JOURNAL	Microb. Pathog.	17 (6),	395-408	(1994)
MEDLINE	95272374			

REFERENCE	1
AUTHORS	Petersson, A., Klarenbeek, V., van Deurzen, J., Poolman, J.T. and Hommessen, V.
TITLE	Molecular characterization of the structural gene for the lactoferrin receptor of the meningococcal strain H44/76
JOURNAL	Microb. Pathog. 17 (6), 395-408 (1994)
MEDLINE	95273374
PUBMED	7752881
REFERENCE	2 (baase 1 to 3398)
AUTHORS	Petersson, A.M.
TITLE	Direct Submision
JOURNAL	Submitted (23-JUN-1994) A.M. Petersson, Dept of Mol Cell Biology Utrecht University, Padualaan 8, 3584 CH Utrecht, NETHERLANDS
FEATURES	Location/Qualifiers
Source	1. .3398

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UNRES      Location/Qualifiers
source      1..3398
             /organism="Neisseria meningitidis"
             /mol_type="genomic DNA"
             /strain="H44/76"
             /db_xref="taxon:487"
             389..408
             /note="putative"
misc_binding /bound_moiety="Pur"
gene        550..3372
             /gene="lbpA"
CDS         550..3372

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Gene      550..3372
/gene="lbpA"
CDS       550..3372
/gene="lbpA"
/codon_start=1
/transl_table=11
/product="lactoferrin binding protein"
/protein_id="CA56233.1"
/db_xref="GI:509054"
/db_xref="GOA:O51187"
/db_xref="UniProt:"EMBL:O51187"
/translation="MNKKSFPPLTLTLALATLAPESYANSSETPAQTOSLKEVTVRAA
KGRSRSEVGLKIVTSETLNKEOVLGRLDRLDPGVAVVEOGNAGSGSIRVY
DKNRVSVGVGVAQIOAFIVQGSLSGCGVGGSGGALIEIYEINI STEYIDKGGSSPH
GSGALGAGVAFRTREADLI SDKSGSWI QAKTVYGSNRPFMKSLGKDEWEGEL
IREROGARETRPHGDIADGVGEYGDRLDARFOTYDIOKKKKVEYFLAESEELKPPA
KLAGNNGYLNKOLNRPWEERKKNKNSLSAEELAVPEAOAHRLNSAQTGGGRILP
DMPDYSGSWLAKLGYRAFGRGHVYGVCFEYTKRKORYDIRDMTEKQYITGEATVPSDKS
GAYDGDPRDGLYFVPIEEKWGDKNLVKGIIGTISRTKFTIDHHRRRRKGLLYREN
EASIDNMADRAVLSFDKQGVATDNTNLTKLCAVYPSVDKCRASADKPYSDSDRH
YREOHNVLNLFEKSLDNKATKHLTLGFGYDASVSRPEQLSHNAARISEFSDVAD
DGKCYKTLGKPEVEVSGCYIEITLRSKGVCPKRIKNSNIHISLDRFSIGKFEDEL
GGGYDKRONFTTSEELVSGSYGTDRSNWSSGVIFSRSHLSLVSRASSGFRPSFOELG
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```

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE
AF022781	<i>Neisseria meningitidis</i> lactoferrin binding protein B (lbpb) gene,	AF022781.1	GI:2843172			<i>Neisseria meningitidis</i>	<i>Neisseria meningitidis</i> 1 (bases 1 to 2277)	Petersson, A., Prinz, T., Umar, A., van der Biezen, J. and Tomassen, J.	Molecular characterization of lbpb, the second lactoferrin-binding protein of <i>Neisseria meningitidis</i>	Microbiol. 27 (3) 599-610 (1998)	98145315

Db 1319 TCAGCGCTTGAAGGCGGTTTTCGGCGATTAAGGCGGAGCTTCCGCGGCTTTAT 1378
 Qy 340 eSerAspAspAspSerValPheAlaGlyLysGlyAsnSerProValProSe 360
 Db 1379 CAGCAAGCAACAGACCGTATTCGGGTATTCGACGCGCAACAAATATACCCCGGCGCTC 1438
 Qy 360 rGlyLysHithrLysLysLeuAspSerLeuLysLysSerValAspGluAlaLysGly 380
 Db 1439 TGAAGAAACACACCAAAATCTTGATTCCTGAAATATTCCTTATAGGCAAGTGTGA 1498
 Qy 380 uAsnProArgProPheAlaLysSerProMetProAspPheGlyYhiAspAspLysLeu 400
 Db 1499 AAATCCCGACCGCTTTCCTATGCGCGATTTGTCATCCGCAAACTCTT 1558
 Qy 400 uValGluGlyYhiGlyLysProLeuValSerGluLysLysThrLysLeuLysAspGly 420
 Db 1559 TGTTCGAAGGCGCATGAATTCCTTGTGTTACCAAGAAACCATGAGCTTCCGACCG 1618
 Qy 420 YArgLysMetThrValSerAlaCysAspAspPheLeuThrYValLysLeuGlyArg 440
 Db 1619 CAGGAAATGACCGTCAGTGTGTTGCGACCTTTTGACCTATGTGAACCTCGAGCGAT 1678
 Qy 440 eLysThrGluArgProAlaAlaLysProLysAlaGluAspGluLysAspSerAspLys 460
 Db 1679 AAAACCGAACCTCCGCGCGCAACCGAGCGAGCGAGATTCGCACTTGA 1738
 Qy 460 PAsnGlyLysGluSerGluAspGluLysGlyAspGluLysGlyYhiThrGluAspAla 480
 Db 1739 TAAATGCGCAAGAAACGAAAGCAAGAAATCGCGATTAAGAAAGCAAGCAAGTGCAGC 1798
 Qy 480 AAlGlyYAspGluLysGluLysGluLysGluLysGluLysGluLysGluLysGluLys 500
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 Qy 500 PGIuAlaGluLysGluLysGluLysGluLysGluLysGluLysGluLysGluLysGlu 520
 Db 1859 CGAAGCTGAAAGCACTTAAGAAAGATCGCGCGAGAAAGCAAGCAAGCAAGCAAGCA 1918
 Qy 520 eLeuProValPProGluLysSerLysGlyArgAspLysLeuLysGlyLysLeu 540
 Db 1919 CCGGCTGTCGCGAGAGCTCTAAAGCAAGATATGACCTTTCTGAAAGATATCCG 1978
 Qy 540 gThrAlaGluLysAsnLysProGluLysGlyLysGlyLysGlyLysGlyLysGlyLys 560
 Db 1979 CACGCGAGAAAGCAATATTCGCGCAACCTGAGAAAGCAAGCAAGCAAGCAAGCAAGCA 2038
 Qy 560 AArgLysGlyLysProLysGluLysAspAsnHisaAspLysGluAlaLysAlaLysAla 580
 Db 2039 GCGATCGGCAAAACCATTCATGGAACATATGCGGATTAAGAAAGCGGCAAAAGCACT 2098
 Qy 580 LPhenThrValAspPheGlyLysLysSerLysGlyThrLeuThrGluLysAsnGly 600
 Db 2099 ATTTACCGTGTATTCGCGCAAGAAATCAATTCGCGAAAGCTGAGCGAGAAAGCAAGCT 2158
 Qy 600 LGIuProAlaPheArgLysGluLysGlyLysGlyLysGlyLysGlyLysGlyLysGly 620
 Db 2159 AGAACCTGCTTTCGATTTGAAGACGCGGTATTCAGGCAAGCTTCCATGCGCAAGC 2218
 Qy 620 AArgThrArgAspAspGlyLysLeuSerGlyLysGlyLysGlyLysGlyLysGlyLys 640
 Db 2219 GCGCACTCGGATACGCGATTCGCGGCAAGGCTTTCGCAAAACCGCAGATCTT 2278
 Qy 640 eLysValAspAspLeuArgValGluGlyLysPheThrGlyProLysAlaGluLysLeu 660
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 Qy 660 YGlyLysLysLysPheAspAsnAspGlyLysSerLeuGlyLysThrGluLysThrGlu 680
 Db 2339 CGGTATTTATTTCAATATATATGAGAAATCTTGTGATTAACGAGTACTGAAATTA 2398
 Qy 680 eValGluAlaAspValAspValAspValAspValAspValAspValAspValAspVal 700
 Db 2399 AGTTGAAGCTGATGTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 2457

Qy 700 LysGluLysProGluValLysProGluPheGlyValAlaLysLysAsp 720
 Db 2458 AACAGTTAAACCTGAGATTAACCCCAATTCGCGGTGTTGCGGAGAAAGATA 2517
 Qy 720 snLysGluValGluLys 725
 Db 2518 ATTAAGAGGTGAGAAAA 2534

RESULT 6
 NMIRQA
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

1. Petersen, A., van der Ley, P., Poolman, J.T. and Tommassen, J. Molecular characterization of the 98-kilodalton iron-regulated outer membrane protein of *Neisseria meningitidis* Infect. Immun. 61(11): 4724-4733 (1993)
 2. (bases 1 to 3171)
 8406871
 Petersen, A.M.
 Direct Submission
 Submitted (17-NOV-1992) A.M. Petersen, University of Utrecht, Padualaan 8, 3584 CH Utrecht, THE NETHERLANDS

FEATURES
 source
 1. 3171
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 /mol_type="genomic DNA"
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 /db_xref="taxon:487"
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 SSDEGSLGAGVAFRTEADLISDEKSWGIQAKTAYGSKRPFMSLIGFSGDG
 EGLIRTERGRERHPHGDADGVAYGINLDAFRQYGIKRYRTEFIDHHRRRMGLY
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 RLPDEPDYDGSWMLAGYRFGGRHYVGVPFDKORXPIRDTETKQYGTDEAKF
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 RYENERSDVMADKAVLSPDKOVATDNNLTAKLCAVPAVDKSCRASADKPYSDS
 DRHYEORHVLNALSPEKSKMKTKHLLTGFGYDASNAISRPEQLSHNAARISEYD
 DYTDDKDKYLGPVEVSGVYIEITLSRKCVPKINSNHSISPEQLSHNAARISEYD
 FSLGGRIDRNKFTISELVASGRYVDSNMGVLPKPNRHSISYASASGFRPSFOE
 LFGLIDYHDPKQMRPALKSEKAAAREIGLOKGRPGLEISFRRRTYDMLAVADH
 KTKLPNOAGQLTEIDRIDYNNOMSLGCVNLGKIDMGVIGKLPBGLYTTLAVNR
 KPSVSNRPGLSIRSYALDAVDSRYLPGFIDPQKMGANIMLTYSKGNDELAY
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 ORIGIN

Alignment Scores:

Pred. No.: 3,766-67 Length: 3171
 Score: 70.00 Matches: 70
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 9.66% Indels: 0
 DB: 1 Gaps: 0

US-10-735-098-2 (1-725) x NMIR0A (1-3171)

OY 656 AAlagIuLeuGlyIleIlePheAaNaAaPGLySseRleuGlyIlethrglu 675
 Db 20 GCGAGGATTCGGCGGATTTATTTCAATATGATGGAATCTTGATTAAGTGA 79
 OY 676 GYthrgluAenLysValGluAlaAspValAspValAspValAspValAspVal 695
 Db 80 GGTACTGAAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 139
 OY 696 AspaAaPvaIGluLeuLysProGluValLysProGluPheGlyValAlaPheGly 715
 Db 140 GATGCTGATTTGAAACAGTTAAACCTTAAGTTAAACCCCAATTCGGCGTATTCGCT 199
 OY 716 AAluLysAspAsnLysGluValLys 725
 Db 200 GCGAGAAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 229

RESULT 7

LOCUS AF123380 2226 bp DNA linear BCT 24-MAY-1999
 DEFINITION Neisseria meningitidis strain H44/76 lactoferrin-binding protein precursor (lbpB) gene, complete cds.
 ACCESSION AF123380
 VERSION AF123380.1 GI:4884686

KEYWORDS

Neisseria meningitidis
 Neisseria meningitidis
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Neisseria.

REFERENCE

1 (bases 1 to 2226)
 Petersen, A., van der Biesen, J., Joosten, V., Hendriksen, J. and Tommaseen, J.
 Sequence variability of the meningococcal lactoferrin-binding protein lbpB

JOURNAL Gene 231 (1-2), 105-110 (1999)
 MEDLINE 99250255
 PUBMED 10231574

2 (bases 1 to 2226)
 Petersen, A., van der Biesen, J., Joosten, V., Hendriksen, J. and Tommaseen, J.
 Direct Submision

TITLE Submitted (26-JAN-1999) Department of Molecular Cell Biology,
 JOURNAL Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands
 FEATURES
 source

1..2226
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 /mol_type="genomic DNA"
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CDS

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 EIWTSNRKQFSNRFGYDGFVYSGEHSQSIPSAQTVQSGNMQYMTDAIRHRTGA
 ADIPQTKARVYGTWEARISKPIQWNAHDKKAAKAFVDVDFEKSISGLTLEKNGVO
 PAFHENGVLKNGFATARTRDGINSNDSTNPSFANNLLVTCGYGQVASEL
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ORIGIN

Alignment Scores:
 Pred. No.: 9,756-53 Length: 2226
 Score: 57.00 Matches: 57
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 7.86% Indels: 0
 DB: 1 Gaps: 0

US-10-735-098-2 (1-725) x AF123380 (1-2226)

OY 1 MetCysLysProAenLYGlyIleValleuLeuProleuLeuAlaSerCysIle 20
 Db 1 ATGTGTAACCGAATATGCGGCGATTCCTTGTCCTTACTTGGCATCTTGATT 60
 OY 21 GYthrgluAenLysValGluAlaAspValAspValAspValAspValAspVal 40
 Db 61 GCGGCAATTCGCGGAGCCGCTGTGTAATCAACGCCGCGGATCCCGTCACT 120

OY 41 PheLysSerLysAspValProThrProProProAlaLysProSerIleGlu 57
 Db 121 TTCAAGCTTAAAGACGTTCCACATCCGCCCTCCCAACTTCTAATGAA 171

RESULT 8

LOCUS A98972 2226 bp DNA linear PAT 26-JAN-2000
 DEFINITION Sequence 5 from Patent WO9909176.
 ACCESSION A98972
 VERSION A98972.1 GI:6781932

KEYWORDS

Neisseria meningitidis
 Neisseria meningitidis
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Neisseria.

REFERENCE

1 (bases 1 to 2226)
 Petersen, A., van der Biesen, J., Joosten, V., Hendriksen, J. and Tommaseen, J.
 Sequence variability of the meningococcal lactoferrin-binding protein lbpB

JOURNAL Gene 231 (1-2), 105-110 (1999)
 MEDLINE 99250255
 PUBMED 10231574

2 (bases 1 to 2226)
 Petersen, A., van der Biesen, J., Joosten, V., Hendriksen, J. and Tommaseen, J.
 Direct Submision

TITLE Submitted (26-JAN-1999) Department of Molecular Cell Biology,
 JOURNAL Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands
 FEATURES
 source

1..2226
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1..2226
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 /db_xref="GI:6781933"

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 EIWTSNRKQFSNRFGYDGFVYSGEHSQSIPSAQTVQSGNMQYMTDAIRHRTGA
 ADIPQTKARVYGTWEARISKPIQWNAHDKKAAKAFVDVDFEKSISGLTLEKNGVO
 PAFHENGVLKNGFATARTRDGINSNDSTNPSFANNLLVTCGYGQVASEL
 GDPSEDLGYLVYGGNVGATSYAATADREGKHPAEYTVDEDKTLTGQLIKQYVOK

Score: 43.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 5.93%
Matches: 43
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-735-098-2 (1-725) x BD074758 (1-2262)

QY 171 ArgLeuGlyTyrAspGlyPheValTyrTyrSerGlyIuArgProSerGlnSerLeuPro 190
DB 526 CGCTTAGTATGACGGCTTTGTATATTCCGAGAACGCTCTTCCCATCTTTACCG 585
QY 191 SerAlaGlyThrAlaGlyTyrSerGlyAsnTyrGlnTyrMetThrAspAlaValArgHis 210
DB 586 AGCGGGAACGGTGGAAATTCGTGACTGGCAATATATGACCGATCCAAACGTCAT 645
QY 211 ArgAlaGly 213
DB 646 CGAGCAGGT 654

RESULT 22
AF072890 2519 bp DNA linear BCT 22-JUN-1999
LOCUS Neisseria gonorrhoeae lactoferrin binding protein B precursor
DEFINITION (lbpB) gene, complete cds.
ACCESSION AF072890
VERSION AF072890.1 GI:4106392
KEYWORDS
SOURCE Neisseria gonorrhoeae
ORGANISM Neisseria gonorrhoeae
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
1 (bases 1 to 2519)
Biswas, G.D., Anderson, J.E., Chen, C.J., Corneliussen, C.N. and
Sparling, P.F.
Identification and functional characterization of the Neisseria
gonorrhoeae lbpB gene product
Infect. Immun. 67 (1), 455-459 (1999)

REFERENCE
AUTHORS
JOURNAL
FEATURES
source
terminator
gene
protein_bind
RBS
CDS

1. (bases 1 to 2519)
Biswas, G.D., Anderson, J.E., Corneliussen, C.N. and Sparling, P.F.
Direct Submission
Submitted (18-JUN-1998) Medicine/ID, Univ. of N. Carolina, 521
Burnett Womack/CB 7030, Chapel Hill, N.C. 27599, USA
Location/Qualifiers
1. 2519
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/mol_type="genomic DNA"
/strain="FA19"
/db_xref="taxon:485"
184..209
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276..2496
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/note="lbpB"
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/transl_table=11
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/protein_id="AAD0809.1"
/db_xref="GI:4106393"
/translation="MRKLNYGIALPLPLMLASCGNGFVOPVSTPTAYPVTKSKD
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DVFVLSKSKKLOQLSEIKHSDVETIRSEKSKKGYEFPVADGAVYVTKNCKDEI
EONSGRKFTHRFGIDGFVYSGRPSQSLPSAGTAVYFNGMOTMTAKRHRTKAVA

442

sig_peptide
mat_peptide
misc_feature
ORIGIN
Alignment Scores:
Pred. No.: 9/22-35
Score: 41.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 5.66%
Matches: 2519
Conservative: 41
Mismatch: 0
Indels: 0
Gaps: 0

US-10-735-098-2 (1-725) x AF072890 (1-2519)
QY 101 GAGGATGATGTTCTGTTTATACGTTCAAAAGAAATTAACCTCAACACTTAAAGC 669
DB 610 GAGGATGATGTTCTGTTTATACGTTCAAAAGAAATTAACCTCAACACTTAAAGC 669
QY 121 GAGGATGATGTTCTGTTTATACGTTCAAAAGAAATTAACCTCAACACTTAAAGC 669
DB 610 GAGGATGATGTTCTGTTTATACGTTCAAAAGAAATTAACCTCAACACTTAAAGC 669
QY 141 Tyr 141
DB 720 TAT 732

RESULT 23
NGU16260
LOCUS NGU16260 3300 bp DNA linear BCT 27-FEB-1996
DEFINITION Neisseria gonorrhoeae lactoferrin receptor precursor (lbpA) gene,
complete cds.
ACCESSION U16260
VERSION U16260.1 GI:915277
KEYWORDS
SOURCE Neisseria gonorrhoeae
ORGANISM Neisseria gonorrhoeae
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
1 (bases 1 to 3300)
Biswas, G.D. and Sparling, P.F.
Characterization of lbpA, the structural gene for a lactoferrin
receptor in Neisseria gonorrhoeae
Infect. Immun. 63 (8), 2958-2967 (1995)

REFERENCE
AUTHORS
JOURNAL
FEATURES
source
terminator
gene
protein_bind
RBS
CDS

Biswas pg1

Biswas
Protect. Pg. 2
Immun.

ACCEDION
VERSION

1000 bp DNA linear PAT 01-MAR-2003
15 from Patent WO0209746.
1 GI:19169587

US-10-735-098-2 (1-725) x AAT11243 (1-2070)

QY 649 G1yG1yPhetYrG1yProLySA1aG1uLcUeUg1yG1y 661
 DB 1912 GGGCGTTTTCAGCGCCCAAGCCGAGAGTTGGCGGA 1950

RESULT 21

AAT11241 standard; DNA; 2114 BP.

AAT11241;

DT 16-OCT-2003 (revised)
 DT 02-SEP-1996 (first entry)

Neisseria meningitidis strain 6940 transferrin receptor Tbp2 gene.

KW Transferrin receptor; Tbp2 subunit; deletion mutant; vaccine;
 KW passive immunisation; immunotherapy; IM2169; ss.

Neisseria meningitidis; (strain 6940).

Key Location/Qualifiers

FT CDS 1..2082
 FT /*tag= a
 FT 1..2079
 FT mat_peptide /*tag= b

W09533049-A2.

07-DEC-1995.

30-MAY-1995; 95MO-FR000701.

31-MAY-1994; 94FR-00006594.

PA (INMR) PASTEUR MERIEUX SERUMS & VACCINS.
 PA (TRGE) TRANSGENE SA.

Millet MBJ, Lissolo L, Mazarin V, Legrain M, Jacobs E;

WPI; 1996-030562/03.

P-PSDB; AAR88646.

Polypeptide(s) for vaccination against Neisseria meningitidis group B - comprising deletion mutants of transferrin receptor Tbp2 subunit.

Disclosure; Page 53-56; 114pp; French.

CC The present sequence is that of the N.meningitidis strain 6940
 CC transferrin Tbp2 subunit gene. The Tbp2 polypeptide has three domains: an
 CC N-terminal domain, a hinge domain and a C-terminal domain; deletion
 CC mutants in which at least one of the domains is partially or totally
 CC deleted are claimed, provided that the first and second domains are not
 CC simultaneously partially or totally deleted. Strain 6940 is an IM2169-
 CC related N.meningitidis strain and the positions of the 3 domains are
 CC defined by alignment with the IM2169 sequence. The deletion mutant
 CC polypeptides of the invention can generate an immune response against
 CC N.meningitidis. (Updated on 16-OCT-2003 to standardise OS field)

Sequence 2114 BP; 695 A; 478 C; 511 G; 430 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.0177 Length: 2114
 Score: 13.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.79% Indels: 0
 DB: 2 Gaps: 0

US-10-735-098-2 (1-725) x AAT11241 (1-2114)

QY 649 G1yG1yPhetYrG1yProLySA1aG1uLcUeUg1yG1y 661

DB 1936 GGGCGTTTTCAGCGCCCAAGCCGAGAGTTGGCGGA 1974

RESULT 22

AAT11242 standard; DNA; 2114 BP.

AAT11242;

DT 16-OCT-2003 (revised)
 DT 02-SEP-1996 (first entry)

Neisseria meningitidis strain S3032 transferrin receptor Tbp2 gene.

KW Transferrin receptor; Tbp2 subunit; deletion mutant; vaccine;
 KW passive immunisation; immunotherapy; IM2169; ss.

Neisseria meningitidis; (strain S3032).

Key Location/Qualifiers

FT CDS 1..2100
 FT /*tag= a
 FT 1..2097
 FT mat_peptide /*tag= b

W09533049-A2.

07-DEC-1995.

30-MAY-1995; 95MO-FR000701.

31-MAY-1994; 94FR-00006594.

PA (INMR) PASTEUR MERIEUX SERUMS & VACCINS.
 PA (TRGE) TRANSGENE SA.

Millet MBJ, Lissolo L, Mazarin V, Legrain M, Jacobs E;

WPI; 1996-030562/03.

P-PSDB; AAR88647.

Polypeptide(s) for vaccination against Neisseria meningitidis group B - comprising deletion mutants of transferrin receptor Tbp2 subunit.

Disclosure; Page 58-61; 114pp; French.

CC The present sequence is that of the N.meningitidis strain S3032
 CC transferrin Tbp2 subunit gene. The Tbp2 polypeptide has three domains: an
 CC N-terminal domain, a hinge domain and a C-terminal domain; deletion
 CC mutants in which at least one of the domains is partially or totally
 CC deleted are claimed, provided that the first and second domains are not
 CC simultaneously partially or totally deleted. Strain S3032 is an IM2169-
 CC related N.meningitidis strain and the positions of the 3 domains are
 CC defined by alignment with the IM2169 sequence. The deletion mutant
 CC polypeptides of the invention can generate an immune response against
 CC N.meningitidis. (Updated on 16-OCT-2003 to standardise OS field)

Sequence 2114 BP; 691 A; 493 C; 509 G; 421 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.0177 Length: 2114
 Score: 13.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.79% Indels: 0
 DB: 2 Gaps: 0

US-10-735-098-2 (1-725) x AAT11242 (1-2114)

QY 649 G1yG1yPhetYrG1yProLySA1aG1uLcUeUg1yG1y 661

DB 1942 GGGCGTTTTCAGCGCCCAAGCCGAGAGTTGGCGGA 1980

Iron uptake protein; transferrin binding protein; TbpA; TbpB; vaccine;
neisserial disease; meningococcal disease; gonococcal disease;
antiflammarory; antibacterial; ds.
Neisseria meningitidis.

Key Location/Qualifiers
CDs 1.2139
/tag= a
/product= "Neisseria meningitidis TbpB protein"

MO20UT173080-A2.
04-OCT-2001.

27-MAR-2001; 2001MO-GB001348.
27-MAR-2000; 2000GB-00007433.

(MICR-) MICROBIOLOGICAL RES AUTHORITY.

Gorringe AR, Hudson MJ, Macheson MA, Robinson A, West DM;
WPI; 2001-616522/71.
P-PSDB; AAE12019.

Non-neisserial cells useful in manufacturing of vaccines without the loss
of antigenicity of the native protein, against meningococcal diseases
such as meningitis, express a recombinant neisserial iron uptake protein.

Example 1; Page 19-21; 57pp; English.

The present invention relates to a non-neisserial cell expressing a
neisserial iron uptake protein, where neisserial iron uptake proteins
including transferrin binding protein (Tbp) A and TbpB can be extracted
from the cell under mild conditions and retains substantially the
antigenicity of native iron uptake protein. The non-neisserial cell is
useful in manufacture of Tbp, and in the manufacture of vaccines for
protection against neisserial disease, meningococcal disease and/or
gonococcal disease. The affinity matrix is useful for purifying a Tbp,
where Tbp containing preparation is eluted through the matrix. The
present sequence is a Neisseria meningitidis strain K454 cpbB gene

Sequence 2139 BP; 696 A; 492 C; 519 G; 432 T; 0 U; 0 Other;

Alignment Scores:
Seq. No.: 0.0179 Length: 2139
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.79% Indels: 0
Gaps: 0

-10-735-098-2 (1-725) x AAD19530 (1-2139)

649 GlyGlyPheTyrglyProlysaIagluGluLeuGlygly 661
1993 GCGCGTTTTCAGGCGCCCAAGCCGAGAGTTGGCGCGA 2031

AA055619 standard; DNA; 2230 BP.

AA055619;

16-OCT-2003 (revised)
25-MAR-2003 (revised)
15-JUL-1994 (first entry)

N meningitidis IM2169 transferrin receptor Tbp2 subunit DNA sequence.

Transferrin receptor; Tbp2 subunit; strain IM2169; meningitis vaccine;



Ja Co 63

Iron transport protein; iron chelator; ss.

Neisseria meningitidis; (strain IM2169).

Key Location/Qualifiers
CDs 60.2195
/tag= a
sig_peptide 60.119
mat_peptide 120.2192
/tag= b
/product= "Tbp2"

FR2692592-A1.
24-DEC-1993.

19-JUN-1992; 92FR-00007493.

19-JUN-1992; 92FR-00007493.

(INMR) PASTEUR MERIEUX SERUMS & VACCINS.
(TRGE) TRANSGENE SA.

Jacobs E, Legrain M, Mazarin V, Bouchon-Theisen B, Shryvers AB;
Bloch M;
WPI; 1994-028254/04.
P-PSDB; AAR48222.

DNA coding for neisseria meningitidis proteins - namely transferrin
receptor subunits.

Claim 2-7 and 11-12; Page 36-40; 60pp; French.

Sequences coding for the Tbp1 and Tbp2 transferrin receptor subunits were
isolated from a Neisseria meningitidis strain IM2169 genomic DNA library
(see AA055618 and AA055619, respectively). Cells transformed with the DNA
can be used for large scale production of the receptor proteins. (Updated
on 25-MAR-2003 to correct PW field.) (Updated on 16-OCT-2003 to
standardise OS field)

Sequence 2230 BP; 727 A; 483 C; 547 G; 473 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.0186 Length: 2230
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.79% Indels: 0
DB: 2 Gaps: 0

US-10-735-098-2 (1-725) x AA055619 (1-2230)

649 GlyGlyPheTyrglyProlysaIagluGluLeuGlygly 661
2037 GCGCGTTTTCAGGCGCCCTTAAGCCGAGAGTTGGCGCGA 2075

AA055619 standard; DNA; 2230 BP.

AA055619;

16-OCT-2003 (revised)
30-AUG-1996 (first entry)

Neisseria meningitidis strain IM2169 transferrin receptor Tbp2 gene.

Transferrin receptor; Tbp2 subunit; deletion mutant; vaccine;
passive immunisation; immunotherapy; ss.
Neisseria meningitidis; (strain IM2169).

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